STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _10/579,104_
Source: _FWP_
Date Processed by STIC: _5/23/06_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT
MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.4.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
          http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
   U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 10/579,104

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1____Wrapped Nucleics
Wrapped Aminos   The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2____Invalid Line Length   The rules require that a line **not exceed** 72 characters in length. This includes white spaces.

3____Misaligned Amino
Numbering   The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.

4____Non-ASCII   The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**

5____Variable Length   Sequence(s)____contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6____PatentIn 2.0
"bug"   A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)_____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

7____Skipped Sequences
(OLD RULES)   Sequence(s)_____ missing. If intentional, please insert the following lines for **each** skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.

8____Skipped Sequences
(NEW RULES)   Sequence(s)_____ missing. If **intentional**, please insert the following lines for **each** skipped sequence.
<210> sequence id number
<400> sequence id number
000

9____Use of n's or Xaa's
(NEW RULES)   Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10____Invalid <213>
Response   Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence. (see item 11 below)

11____Use of <220>   Sequence(s)_____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules

12____PatentIn 2.0
"bug"   Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13____ Misuse of n/Xaa   "n" can **only** represent a single nucleotide; "Xaa" can **only** represent a single amino acid

AMC – STIC Systems Branch – 03/02/06

IFWP

```
          RAW SEQUENCE LISTING              DATE: 05/23/2006
          PATENT APPLICATION:  US/10/579,104    TIME: 14:05:52

          Input Set : A:\753-65 PCT-US Sequence Listing.txt
          Output Set: N:\CRF4\05232006\J579104.raw

     3 <110> APPLICANT: POLYPHOR LTD.
     5 <120> TITLE OF INVENTION: Template fixed beta-hairpin mimetics and their use in
     6        phage display
     8 <130> FILE REFERENCE: P1338PCT
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/579,104
C--> 11 <141> CURRENT FILING DATE: 2006-05-12
    13 <160> NUMBER OF SEQ ID NOS: 44
    15 <170> SOFTWARE: PatentIn Ver. 2.1

ERRORED SEQUENCES

   729 <210> SEQ ID NO: 43
   730 <211> LENGTH: 16
   731 <212> TYPE: PRT
   732 <213> ORGANISM: Artificial Sequence
W--> 733 <220> FEATURE:
   733 <223> OTHER INFORMATION: Cysteine residues in positions 3 and 14 are linked
   734        by a disulfide bridge
E--> 736 <400> SEQUENCE: 43
W--> 737 Glu Thr Cys Xaa Xaa Xaa Arg Gly Asp Xaa Xaa Xaa Xaa Xaa Thr Lys
   738  1               5                   10                  15
```

Handwritten annotations:
- Suggestion: Consult Sequence Rules
- pp 1-6
- needs explanation
- in <220>-<223> section
- Does Not Comply Corrected Diskette Needed
- <220> insert this mandatory numeric identifier
- ?
- Xaa's need explanation in <220>-<223> section
- Xaa is at position 14

SEQUENCE LISTING

replace with ↓

<110> POLYPHOR LTD.

<120> Template fixed beta-hairpin mimetics and their use in phage display

<130> P1338PCT

<150> <140> PCT/EP 03/12783
<151> <141> 2003-11-15

These are prior data

```
<210> 1
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: key sequence

<400> 1
Val Arg Lys Lys
  1
```

insufficient explanation – give source (see item 11 on Error Summary Sheet)

This type of error appears in subsequent sequences, too.

<210> 42
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:DNA sequence of
      randomized template fixed beta-hairpin mimetic
      Phage library

<220>
<221> CDS
<222> (1)..(48)

<220>
<223> Xaa in the peptide chain signifies randomized
      amino acid positions

<220>
<223> Cysteine residues in positions 3 and 14 are linked
      by a disulfide bridge

<400> 42
gaa acc tgc nnk nnk nnk cgt ggt gac nnk nnk nnk nnk thc acc aaa   48

h's need explanation in <220>-<223> section

<210> 44
<211> 84
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:olignucleotide
     for library construction

<400> 44
catgtttcgg ccgagccacc acctttggtg camnnnnnnn nnnngtcacc acgmnnnnnn 60
nngcaggttt cagagtgaga atag 84

n's need explanation

Input Set : **A:\753-65 PCT-US Sequence Listing.txt**
Output Set: **N:\CRF4\05232006\J579104.raw**

<u>Use of n's or Xaa's(NEW RULES):</u>
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
in <220> to <223> section, please explain location of n or Xaa, and which
residue n or Xaa represents.

Seq#:7; Xaa Pos. 4,5
Seq#:42; N Pos. 10,11,13,14,16,17,28,29,31,32,34,35,37,38
Seq#:42; Xaa Pos. 4,5,6,10,11,12,13,14
Seq#:43; Xaa Pos. 4,5,6,10,11,12,13,14
Seq#:44; N Pos. 34,35,37,38,40,41,43,44,55,56,58,59,61,62

VERIFICATION SUMMARY   DATE: 05/23/2006
PATENT APPLICATION: **US/10/579,104**   TIME: 14:05:53

            Input Set : **A:\753-65 PCT-US Sequence Listing.txt**
            Output Set: **N:\CRF4\05232006\J579104.raw**

L:10 M:270 C: Current Application Number differs, Replaced Current Application Number
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:114 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:7
L:114 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:7
L:114 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:0
L:724 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:42 after pos.:0
M:341 Repeated in SeqNo=42
L:733 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:43
L:736 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:43
L:737 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:43
L:737 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:43
L:737 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43 after pos.:0
L:752 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:44
L:752 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:44
L:752 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:44 after pos.:0
M:341 Repeated in SeqNo=44